



SEQUENCE LISTING

<110> Behl, Christian
Klostermann, Andreas

<120> Human semaphorin 6A-1 (SEMA6A-A), a gene involved in neuronal development and regeneration mechanisms during apoptosis, and its use as a potential drug target

<130> 48498-0100 (48498-258443)

<140> US 09/856,681
<141> 2001-08-03

<150> PCT/EP99/09215
<151> 1999-11-26

<150> EP 98122441.3
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<170> PatentIn version 3.2

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gga atg gcc aga tgc cca tat gat gcc aaa cat gcc aac gtt gca ctg Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu 165 170 175	1185
ttt gca gat gga aaa cta tac tca gcc aca gtg act gac ttc ctt gcc Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala 180 185 190	1233
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gtt tgt aag aat gat atg gga gga tct caa aga gtc ctg gag aaa cag Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln 260 265 270	1473
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tct cat ttt tat ttc aac att ctc cag gca gtt aca gat gtg att cgt Ser His Phe Tyr Phe Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg 290 295 300	1569
atc aac ggg cgt gat gtt gtc ctg gca acg ttt tct aca cct tat aac Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn 305 310 315 320	1617
agc atc cct ggg tct gca gtc tgt gcc tat gac atg ctt gac att gcc Ser Ile Pro Gly Ser Ala Val Cys Ala Tyr Asp Met Leu Asp Ile Ala 325 330 335	1665

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Trp Thr Pro Val Pro Asp Glu Arg Val Pro Lys Pro Arg Pro Gly Cys	
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Cys Ala Gly Ser Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe	
370 375 380	
cct gat gat acc ctg aac ttc atc aag acg cac ccg ctc atg gat gag	1857
Pro Asp Asp Thr Leu Asn Phe Ile Lys Thr His Pro Leu Met Asp Glu	
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Arg Tyr Arg Leu Thr Lys Ile Ala Val Asp Thr Ala Ala Gly Pro Tyr	
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Gln Asn His Thr Val Val Phe Leu Gly Ser Glu Lys Gly Ile Ile Leu	
435 440 445	
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Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu	
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ttc ctg gag gag atg agt gtt tac aac tct gaa aaa tgc agc tat gat	2097
Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp	
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Gly Val Glu Asp Lys Arg Ile Met Gly Met Gln Leu Asp Arg Ala Ser	
485 490 495	
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Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu	
500 505 510	
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Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser	
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Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His	

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gct caa gag ggg tat gag tct agg gga gga atg ctg gac tgg aag cat Ala Gln Glu Gly Tyr Glu Ser Arg Gly Gly Met Leu Asp Trp Lys His 595 600 605			2481
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ctg gct ttc gtc atg ggg gcc gtc ttc tgg gcc atc acc gtc tac tgc Leu Ala Phe Val Met Gly Ala Val Phe Ser Gly Ile Thr Val Tyr Cys 660 665 670			2673
gtc tgt gat cat cgg cgc aaa gac gtg gct gtg gtg cag cgc aag gag Val Cys Asp His Arg Arg Lys Asp Val Ala Val Val Gln Arg Lys Glu 675 680 685			2721
aag gag ctc acc cac tgc cgc cgg gcc tcc atg agc agc gtc acc aag Lys Glu Leu Thr His Ser Arg Arg Gly Ser Met Ser Ser Val Thr Lys 690 695 700			2769
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gcc atc ctc acg cca ctc atg cac aac ggc aag ctc gcc act ccc ggc Ala Ile Leu Thr Pro Leu Met His Asn Gly Lys Leu Ala Thr Pro Gly 725 730 735			2865
aac acg gcc aag atg ctc att aaa gca gac cag cac cac ctg gac ctg			2913

Asn Thr Ala Lys Met Leu Ile Lys Ala Asp Gln His His Leu Asp Leu	
740 745 750	
acg gcc ctc ccc acc cca gag tca acc cca acg ctg cag cag aag cgg	2961
Thr Ala Leu Pro Thr Pro Glu Ser Thr Pro Thr Leu Gln Gln Lys Arg	
755 760 765	
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Lys Pro Ser Arg Gly Ser Arg Glu Trp Glu Arg Asn Gln Asn Leu Ile	
770 775 780	
aat gcc tgc aca aag gac atg ccc ccc atg gcc tcc cct gtg att ccc	3057
Asn Ala Cys Thr Lys Asp Met Pro Pro Met Gly Ser Pro Val Ile Pro	
785 790 795 800	
acg gac ctg ccc ctg cgg gcc tcc ccc agc cac atc ccc agc gtg gtg	3105
Thr Asp Leu Pro Leu Arg Ala Ser Pro Ser His Ile Pro Ser Val Val	
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Val Leu Pro Ile Thr Gln Gln Gly Tyr Gln His Glu Tyr Val Asp Gln	
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ccc aaa atg agc gag gtg gcc cag atg gcg ctg gag gac cag gcc gcc	3201
Pro Lys Met Ser Glu Val Ala Gln Met Ala Leu Glu Asp Gln Ala Ala	
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aca ctg gag tat aag acc atc aag gaa cat ctc agc agc aag agt ccc	3249
Thr Leu Glu Tyr Lys Thr Ile Lys Glu His Leu Ser Ser Lys Ser Pro	
850 855 860	
aac cat ggg gtg aac ctt gtg gag aac ctg gac agc ctg ccc ccc aaa	3297
Asn His Gly Val Asn Leu Val Glu Asn Leu Asp Ser Leu Pro Pro Lys	
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gtt cca cag cgg gag gcc tcc ctg ggt ccc cgg gga gcc tcc ctg tct	3345
Val Pro Gln Arg Glu Ala Ser Leu Gly Pro Pro Gly Ala Ser Leu Ser	
885 890 895	
cag acc ggt cta agc aag cgg ctg gaa atg cac cac tcc tct tcc tac	3393
Gln Thr Gly Leu Ser Lys Arg Leu Glu Met His His Ser Ser Ser Tyr	
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ggg gtt gac tat aag agg agc tac ccc acg aac tgg ctc acg aga agc	3441
Gly Val Asp Tyr Lys Arg Ser Tyr Pro Thr Asn Ser Leu Thr Arg Ser	
915 920 925	
cac cag gcc acc act ctc aaa aga aac aac act aac tcc tcc aat tcc	3489
His Gln Ala Thr Thr Leu Lys Arg Asn Asn Thr Asn Ser Ser Asn Ser	
930 935 940	

tct cac ctc tcc aga aac cag agc ttt ggc agg gga gac aac ccg ccg 3537
 Ser His Leu Ser Arg Asn Gln Ser Phe Gly Arg Gly Asp Asn Pro Pro
 945 950 955 960

ccc gcc ccg cag agg gtg gac tcc atc cag gtg cac agc tcc cag cca 3585
 Pro Ala Pro Gln Arg Val Asp Ser Ile Gln Val His Ser Ser Gln Pro
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 Ser Gly Gln Ala Val Thr Val Ser Arg Gln Pro Ser Leu Asn Ala Tyr
 980 985 990

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 Asn Ser Leu Thr Arg Ser Gly Leu Lys Arg Thr Pro Ser Leu Lys Pro
 995 1000 1005

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 Asp Val Pro Pro Lys Pro Ser Phe Ala Pro Leu Ser Thr Ser Met
 1010 1015 1020

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 Lys Pro Asn Asp Ala Cys Thr
 1025 1030

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Gly Ala Gly Phe Pro Glu Asp Ser Glu Pro Ile Ser Ile Ser His Gly
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 35 40 45

Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met
 50 55 60

Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp
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Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr
85 90 95

Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys
100 105 110

His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn
115 120 125

Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys
130 135 140

Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser
145 150 155 160

Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu
165 170 175

Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala
180 185 190

Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg
195 200 205

Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln
210 215 220

Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Phe Arg Glu Ile Ala
225 230 235 240

Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln
245 250 255

Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln
260 265 270

Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp
 275 280 285

Ser His Phe Tyr Phe Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg
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Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn
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Ser Ile Pro Gly Ser Ala Val Cys Ala Tyr Asp Met Leu Asp Ile Ala
 325 330 335

Ser Val Phe Thr Gly Arg Phe Lys Glu Gln Lys Ser Pro Asp Ser Thr
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Trp Thr Pro Val Pro Asp Glu Arg Val Pro Lys Pro Arg Pro Gly Cys
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Cys Ala Gly Ser Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe
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Ala Val Pro Ser Ile Phe Asn Arg Pro Trp Phe Leu Arg Thr Met Val
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Arg Tyr Arg Leu Thr Lys Ile Ala Val Asp Thr Ala Ala Gly Pro Tyr
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Gln Asn His Thr Val Val Phe Leu Gly Ser Glu Lys Gly Ile Ile Leu
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Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu
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Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp

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Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu						
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Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser						
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Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His						
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Leu Ser Pro Asn Ser Arg Leu Thr Phe Glu Gln Asp Ile Glu Arg Gly						
	545			550		555
Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn						
	565			570		575
Gly His Ser Ser Ser Leu Leu Pro Ser Thr Thr Thr Ser Asp Ser Thr						
	580			585		590
Ala Gln Glu Gly Tyr Glu Ser Arg Gly Gly Met Leu Asp Trp Lys His						
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Leu Leu Asp Ser Pro Asp Ser Thr Asp Pro Leu Gly Ala Val Ser Ser						
	610			615		620
His Asn His Gln Asp Lys Lys Gly Val Ile Arg Glu Ser Tyr Leu Lys						
	625			630		635
Gly His Asp Gln Leu Val Pro Val Thr Leu Leu Ala Ile Ala Val Ile						
	645			650		655
Leu Ala Phe Val Met Gly Ala Val Phe Ser Gly Ile Thr Val Tyr Cys						
	660			665		670

Val Cys Asp His Arg Arg Lys Asp Val Ala Val Val Gln Arg Lys Glu
675 680 685

Lys Glu Leu Thr His Ser Arg Arg Gly Ser Met Ser Ser Val Thr Lys
690 695 700

Leu Ser Gly Leu Phe Gly Asp Thr Gln Ser Lys Asp Pro Lys Pro Glu
705 710 715 720

Ala Ile Leu Thr Pro Leu Met His Asn Gly Lys Leu Ala Thr Pro Gly
725 730 735

Asn Thr Ala Lys Met Leu Ile Lys Ala Asp Gln His His Leu Asp Leu
740 745 750

Thr Ala Leu Pro Thr Pro Glu Ser Thr Pro Thr Leu Gln Gln Lys Arg
755 760 765

Lys Pro Ser Arg Gly Ser Arg Glu Trp Glu Arg Asn Gln Asn Leu Ile
770 775 780

Asn Ala Cys Thr Lys Asp Met Pro Pro Met Gly Ser Pro Val Ile Pro
785 790 795 800

Thr Asp Leu Pro Leu Arg Ala Ser Pro Ser His Ile Pro Ser Val Val
805 810 815

Val Leu Pro Ile Thr Gln Gln Gly Tyr Gln His Glu Tyr Val Asp Gln
820 825 830

Pro Lys Met Ser Glu Val Ala Gln Met Ala Leu Glu Asp Gln Ala Ala
835 840 845

Thr Leu Glu Tyr Lys Thr Ile Lys Glu His Leu Ser Ser Lys Ser Pro
850 855 860

Asn His Gly Val Asn Leu Val Glu Asn Leu Asp Ser Leu Pro Pro Lys
865 870 875 880

Pro Pro Pro Ala Pro Gln Arg Val Asp Ser Ile Gln Val His Ser Ser
1 5 10 15

Gln Pro Ser Gly Gln Ala Val Thr Val Ser Arg Gln Pro Ser Leu Asn
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Ala Tyr Asn Ser Leu Thr Arg Ser Gly Leu Lys Arg Thr Pro Ser Leu
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Thr Gln Pro Arg Gly Pro Leu Ser Gln Ala Pro Thr Pro Ala Pro Lys
 35 40 45

Phe Ala Pro Val Ala Pro Lys Phe Thr Pro Val Val Ser Lys Phe Ser
 50 55 60

Pro
 65